

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 10/768,951B
Source: 1 Fw/16
Date Processed by STIC: 11/9/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 11/09/2006

PATENT APPLICATION: US/10/768,951B

TIME: 10:51:39

Input Set : A:\71914.ST25.txt

Output Set: N:\CRF4\11092006\J768951B.raw

3 <110> APPLICANT: COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
 5 <120> TITLE OF INVENTION: STABLE GENE VARIANTS OF LIPASES
 7 <130> FILE REFERENCE: 71914
 9 <140> CURRENT APPLICATION NUMBER: US 10/768,951B
 10 <141> CURRENT FILING DATE: 2004-01-29
 12 <160> NUMBER OF SEQ ID NOS: 22
 14 <170> SOFTWARE: PatentIn version 3.3
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 181
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Bacillus subtilis
 22 <220> FEATURE:
 W--> 23 <221> NAME/KEY: AMINO ACIDS
 24 <222> LOCATION: (1)..(181)
 25 <223> OTHER INFORMATION: enzyme sequence
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 30 1 5 10 15
 33 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
 34 20 25 30
 37 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
 38 35 40 45
 41 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
 42 50 55 60
 45 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly
 46 65 70 75 80
 49 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
 50 85 90 95
 53 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
 54 100 105 110
 57 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
 58 115 120 125
 61 Ile Tyr Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
 62 130 135 140
 65 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
 66 145 150 155 160
 69 Tyr Ser Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
 70 165 170 175
 73 Gly Gln Asn Thr Asn
 74 180
 77 <210> SEQ ID NO: 2
 78 <211> LENGTH: 181
 79 <212> TYPE: PRT

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80 <213> ORGANISM: Bacillus subtilis
83 <220> FEATURE:
W--> 84 <221> NAME/KEY: Amino acid
85 <222> LOCATION: (1)..(181)
86 <223> OTHER INFORMATION: Protein sequence
88 <400> SEQUENCE: 2
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94 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
95          20          25          30
98 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
99          35          40          45
102 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
103          50          55          60
106 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly
107 65          70          75          80
110 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
111          85          90          95
114 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
115          100          105          110
118 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
119          115          120          125
122 Ile Tyr Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
123          130          135          140
126 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
127 145          150          155          160
130 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
131          165          170          175
134 Gly Gln Asn Thr Asn
135          180
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144 <220> FEATURE:
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146 <222> LOCATION: (1)..(181)
147 <223> OTHER INFORMATION: Protein sequence
149 <400> SEQUENCE: 3
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152 1          5          10          15
155 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
156          20          25          30
159 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
160          35          40          45
163 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
164          50          55          60
167 Asp Glu Thr Gly Val Lys Lys Val Asp Ile Val Ala His Ser Met Gly
168 65          70          75          80

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171 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
172      85      90      95
175 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
176      100      105      110
179 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
180      115      120      125
183 Ile Tyr Ser Ser Asp Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
184      130      135      140
187 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
188 145      150      155      160
191 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
192      165      170      175
195 Gly Gln Asn Thr Asn
196      180

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200 <211> LENGTH: 181

201 <212> TYPE: PRT

202 <213> ORGANISM: Bacillus subtilis

205 <220> FEATURE:

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207 <222> LOCATION: (1)..(181)

208 <223> OTHER INFORMATION: Protein Sequence

210 <400> SEQUENCE: 4

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216 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
217      20      25      30
220 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
221      35      40      45
224 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
225      50      55      60
228 Asp Glu Thr Gly Thr Lys Lys Val Asp Ile Val Ala His Ser Met Gly
229 65      70      75      80
232 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
233      85      90      95
236 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
237      100      105      110
240 Lys Ala Pro Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
241      115      120      125
244 Ile Tyr Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
245      130      135      140
248 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
249 145      150      155      160
252 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
253      165      170      175
256 Gly Gln Asn Thr Asn
257      180
260 <210> SEQ ID NO: 5
261 <211> LENGTH: 181

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262 <212> TYPE: PRT
263 <213> ORGANISM: Bacillus subtilis
266 <220> FEATURE:
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268 <222> LOCATION: (1)..(181)
269 <223> OTHER INFORMATION: Protein Sequence
271 <400> SEQUENCE: 5
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277 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
278          20          25          30
281 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
282          35          40          45
285 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
286          50          55          60
289 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly
290 65          70          75          80
293 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
294          85          90          95
297 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
298          100         105         110
301 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
302          115         120         125
305 Ile Tyr Ser Ser Asp Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
306          130         135         140
309 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
310 145         150         155         160
313 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
314          165         170         175
317 Gly Gln Asn Thr Asn
318          180
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327 <220> FEATURE:
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329 <222> LOCATION: (1)..(181)
330 <223> OTHER INFORMATION: Protein sequence
332 <400> SEQUENCE: 6
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335 1          5          10          15
338 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
339          20          25          30
342 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
343          35          40          45
346 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
347          50          55          60
350 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly

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Input Set : A:\71914.ST25.txt

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351 65          70          75          80
354 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
355          85          90          95
358 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
359          100          105          110
362 Lys Ala Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
363          115          120          125
366 Ile Tyr Ser Ser Asp Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
367          130          135          140
370 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
371 145          150          155          160
374 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
375          165          170          175
378 Gly Gln Asn Thr Asn
379          180
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383 <211> LENGTH: 181
384 <212> TYPE: PRT
385 <213> ORGANISM: Bacillus subtilis
388 <220> FEATURE:
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390 <222> LOCATION: (1)..(181)
391 <223> OTHER INFORMATION: Protein sequence
393 <400> SEQUENCE: 7
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396 1          5          10          15
399 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
400          20          25          30
403 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
404          35          40          45
407 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
408          50          55          60
411 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly
412 65          70          75          80
415 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
416          85          90          95
419 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
420          100          105          110
423 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
424          115          120          125
427 Ile Tyr Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
428          130          135          140
431 Asp Gly Ala Ser Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
432 145          150          155          160
435 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
436          165          170          175
439 Gly Gln Asn Thr Asn
440          180
443 <210> SEQ ID NO: 8

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VERIFICATION SUMMARY

DATE: 11/09/2006

PATENT APPLICATION: US/10/768,951B

TIME: 10:51:40

Input Set : A:\71914.ST25.txt

Output Set: N:\CRF4\11092006\J768951B.raw

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L:145 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:206 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:267 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
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L:572 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
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L:694 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12